SEQUENCE LISTING

<110> University of Rochester Fay, Philip J. Wakabayashi, Hironao <120> RECOMBINANT FACTOR VIII HAVING INCREASED SPECIFIC ACTIVITY <130> 176/61701 <140> <141> <150> 60/526,664 <151> 2003-12-03 <160> 7 <170> PatentIn Ver. 2.1 <210> 1 <211> 6999 <212> DNA <213> Human <400> 1 qccaccagaa qatactacct qqqtgcagtg gaactgtcat gggactatat gcaaagtgat 60 ctcggtgagc tgcctgtgga cgcaagattt cctcctagag tgccaaaatc ttttccattc 120 aacacctcag tcgtgtacaa aaagactctg tttgtagaat tcacggatca ccttttcaac 180 atcgctaagc caaggccacc ctggatgggt ctgctaggtc ctaccatcca ggctgaggtt 240 tatgatacag tggtcattac acttaagaac atggcttccc atcctgtcag tcttcatgct 300 gttggtgtat cctactggaa agcttctgag ggagctgaat atgatgatca gaccagtcaa 360 agggagaaag aagatgataa agtcttccct ggtggaagcc atacatatgt ctggcaggtc 420 ctgaaagaga atggtccaat ggcctctgac ccactgtgcc ttacctactc atatctttct 480 catgtggacc tggtaaaaga cttgaattca ggcctcattg gagccctact agtatgtaga 540 gaagggagtc tggccaagga aaagacacag accttgcaca aatttatact actttttgct 600 gtatttgatg aagggaaaag ttggcactca gaaacaaaga actccttgat gcaggatagg 660 gatgctgcat ctgctcgggc ctggcctaaa atgcacacag tcaatggtta tgtaaacagg 720 tctctgccag gtctgattgg atgccacagg aaatcagtct attggcatgt gattggaatg 780 ggcaccactc ctgaagtgca ctcaatattc ctcgaaggtc acacatttct tgtgaggaac 840 catcgccagg cgtccttgga aatctcgcca ataactttcc ttactgctca aacactcttg 900 atggaccttg gacagtttct actgttttgt catatctctt cccaccaaca tgatggcatg 960 gaagettatg teaaagtaga eagetgteea gaggaaceee aactaegaat gaaaaataat 1020 qaaqaagcgg aagactatga tgatgatctt actgattctg aaatggatgt ggtcaggttt 1080 gatgatgaca actotoctto otttatocaa attogotoag ttgocaagaa goatootaaa 1140 acttgggtac attacattgc tgctgaagag gaggactggg actatgctcc cttagtcctc 1200

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Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro 50 55 60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val 65 70 75 80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
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Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala 100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val 115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn 130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser 145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu 165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu 180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser

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725 730 735

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- Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro 785 790 795 800
- His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe 805 810 815
- Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser 820 825 830
- Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val 835 840 845
- Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly 850 855 860
- Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser 865 870 875 880
- Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala 885 890 895
- Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His 900 905 910
- Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro 915 920 925
- Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp 930 935 940
- Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp 945 950 955 950
- Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys 965 970 975
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980 985 990

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Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val 1140 1145 1150

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Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr 1220 1225 1230

Arg Gln Asn Val Glu Gly Ser Tyr Glu Gly Ala Tyr Ala Pro Val Leu

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- Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp 1825 1830 1835 1840
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- Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile 2065 2070 2075 2080
- Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu 2085 2090 2095
- Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp 2100 2105 2110
- Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly 2115 2120 2125
- Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile 2130 2135 2140
- Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser 2145 2150 2155 2160
- Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met 2165 2170 2175
- Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala 2180 2185 2190
- Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala 2195 2200 2205
- Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn 2210 2215 2220
- Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val 2225 2230 2235 2240
- Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr 2245 2250 2255
- Val Lys Glu Phe Leu Ile Ser Ser Gln Asp Gly His Gln Trp Thr

2260 2265 2270

Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp 2275 2280 2285

Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg 2290 2295 2300

Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg 2305 2310 2315 2320

Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr 2325 2330

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